10/709,436

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*** YOU HAVE NEW MAIL ***

=> s polymerase chain reaction and sequencing
L1       114221 POLYMERASE CHAIN REACTION AND SEQUENCING

=> s l1 and nucleotide(4a) label
L2          833 L1 AND NUCLEOTIDE(4A) LABEL

=> s l2 and free (2a) 3 (2a) hydroxyl
L3           30 L2 AND FREE (2A) 3 (2A) HYDROXYL

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4           30 DUP REM L3 (0 DUPLICATES REMOVED)

=> s l4 and (support or substrate)
L5           28 L4 AND (SUPPORT OR SUBSTRATE)

=> d l5 bib abs 1-28

L5   ANSWER 1 OF 28  USPATFULL on STN
AN     2007:147528  USPATFULL
TI     Method of preparing libraries of template polynucleotides
IN     Gormley, Niall Anthony, Nr. Saffron Waldon, UNITED KINGDOM
       Smith, Geoffrey Paul, Nr. Saffron Waldon, UNITED KINGDOM
       Bentley, David, Nr. Saffron Waldon, UNITED KINGDOM
       Rigatti, Roberto, Nr. Saffron Waldon, UNITED KINGDOM
PI     US 2007128624       A1  20070607
AI     US 2006-486953      A1  20060714 (11)
PRAI   GB 2005-22310       20051101
DT     Utility
FS     APPLICATION
LREP   KLAUBER & JACKSON, 411 HACKENSACK AVENUE, HACKENSACK, NJ, 07601, US
CLMN   Number of Claims: 29
ECL    Exemplary Claim: 1
DRWN   12 Drawing Page(s)
LN.CNT 2068
AB     The present invention relates to a method for preparing a library of
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template polynucleotides and use thereof in methods of solid-phase nucleic acid amplification. More specifically, the invention relates to a method for preparing a library of template polynucleotides that have common sequences at their 5' ends and at their 3' ends.

L5 ANSWER 2 OF 28 USPATFULL on STN
AN 2007:55807 USPATFULL
TI Mutant polymerases for sequencing and genotyping
IN Williams, John G.K., Lincoln, NE, UNITED STATES
Anderson, Jon P., Lincoln, NE, UNITED STATES
Urlacher, Teresa M., Wahoo, NE, UNITED STATES
Steffens, David L., Lincoln, NE, UNITED STATES
PA LI-COR, INC., Lincoln, NE, UNITED STATES (U.S. corporation)
PI US 2007048748 A1 20070301
AI US 2005-234677 A1 20050923 (11)
PRAI US 2004-626552P 20041110 (60)
US 2004-613560P 20040924 (60)
DT Utility
FS APPLICATION
LREP TOWNSEND AND TOWNSEND AND CREW, LLP, TWO EMBARCADERO CENTER, EIGHTH FLOOR, SAN FRANCISCO, CA, 94111-3834, US
CLMN Number of Claims: 72
ECL Exemplary Claim: 1
DRWN 13 Drawing Page(s)
LN.CNT 1823
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to the discovery of novel mutant DNA polymerases that possess altered kinetics for incorporating phosphate-labeled nucleotides during polymerization. The invention further relates to the use of these mutant DNA polymerases in sequencing and genotyping methods.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 3 OF 28 USPATFULL on STN
AN 2006:281499 USPATFULL
TI Modified polymerases for improved incorporation of nucleotide analogues
IN Smith, Geoffrey Paul, Essex, UNITED KINGDOM
Bailey, David Mark Dunstan, Essex, UNITED KINGDOM
Sanches, Raquel Maria, Essex, UNITED KINGDOM
Swerdlow, Harold, Essex, UNITED KINGDOM
Earnshaw, David James, Essex, UNITED KINGDOM
PI US 2006240439 A1 20061026
AI US 2004-571706 A1 20040910 (10)
WO 2004-GB3891 20040910
20060608 PCT 371 date
PRAI GB 2003-21306 20030911
DT Utility
FS APPLICATION
LREP KLAUBER & JACKSON, 411 HACKENSACK AVENUE, HACKENSACK, NJ, 07601, US
CLMN Number of Claims: 66
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 4088
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to modified polymerase enzymes which exhibit improved incorporation of nucleotide analogues bearing substituents at the 3' position of the sugar moiety that are larger in size than the naturally occurring 3' hydroxyl group. Also described are methods of using the polymerases to incorporate nucleotides into polynucleotides, particularly in the context of DNA sequencing.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 4 OF 28 USPATFULL on STN
AN 2006:46812 USPATFULL
TI Methods of manipulating nucleic acids
IN Xiang, Charlie, Germantown, MD, UNITED STATES
Brownstein, Michael J., Rockville, MD, UNITED STATES
PA The Gov. of the USA as represented by the Secretary of the Dept. of Health & Human Services (U.S. government)
PI US 2006040283 A1 20060223
AI US 2005-104737 A1 20050411 (11)
RLI Continuation-in-part of Ser. No. WO 2003-US33319, filed on 10 Oct 2003, PENDING Continuation of Ser. No. US 2002-269515, filed on 11 Oct 2002, PENDING Continuation-in-part of Ser. No. WO 2002-US11656, filed on 11 Apr 2002, PENDING
PRAI US 2001-283423P 20010411 (60)
DT Utility
FS APPLICATION
LREP KLARQUIST SPARKMAN, LLP, 121 S.W. SALMON STREET, SUITE #1600, ONE WORLD TRADE CENTER, PORTLAND, OR, 97204-2988, US
CLMN Number of Claims: 46
ECL Exemplary Claim: 1
DRWN 14 Drawing Page(s)
LN.CNT 3952
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods are provided for labeling nucleic acid molecules for use in hybridization reactions, and kits employing these methods. The level of labeling is increased by including one or more reactive modifications, such as amine-modifications, into the primers used to initiate synthesis of the nucleic acid molecule, for instance through random-primed reverse transcription. Also provided are modified random primers (such as amine-modified random primers) useful in these methods, labeling and hybridization kits comprising such primers, labeled nucleic acid molecules and mixtures of molecules, and methods for using them. Methods are also provided for amplifying a nucleic acid template contained within extremely small samples, in some cases as little as one cell. In particular embodiments, a single random primer is used for all steps of the amplification method. The nucleic acid template can either be of cellular or viral origin. The disclosure also provides an improved method of fixing cells, tissue sections, or laser microdissected sections from which RNA can be obtained for subsequent use as RNA templates or for generating labeled probe.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 5 OF 28 USPATFULL on STN
AN 2005:298944 USPATFULL
TI Methods and devices for sequencing nucleic acids
IN Lapidus, Stanley N., Bedford, NH, UNITED STATES
PI US 2005260609 A1 20051124
AI US 2004-852028 A1 20040524 (10)
DT Utility
FS APPLICATION
LREP PROSKAUER ROSE LLP, ONE INTERNATIONAL PLACE 14TH FL, BOSTON, MA, 02110, US
CLMN Number of Claims: 23
ECL Exemplary Claim: 1
DRWN 6 Drawing Page(s)
LN.CNT 788
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides methods and devices for high throughput single molecule sequencing of a plurality of target nucleic acids using a universal primer. Devices of the invention comprise a plurality of oligonucleotides, each having the same sequence, bound to a solid support, and ligated to a plurality of target nucleic acids.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 6 OF 28 USPATFULL on STN
AN 2005:254810 USPATFULL
TI Modified random primers for probe labeling
IN Xiang, Charlie, Germantown, MD, UNITED STATES
Brownstein, Michael J, Rockville, MD, UNITED STATES
PI US 2005221304 A1 20051006
AI US 2003-474611 A1 20020411 (10)
WO 2002-US11656 20020411
20031009 PCT 371 date
PRAI US 2001-283423P 20010411 (60)
DT Utility
FS APPLICATION
LREP KLARQUIST SPARKMAN, LLP, 121 S.W. SALMON STREET, SUITE #1600, ONE WORLD TRADE CENTER, PORTLAND, OR, 97204-2988, US
CLMN Number of Claims: 33
ECL Exemplary Claim: 1
DRWN 5 Drawing Page(s)
LN.CNT 2783
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods are provided for labeling nucleic acid molecules for use in hybridization reactions, and kits employing these methods. The level of labeling is increased by including one or more reactive modifications, such as amine-modifications, into the primers used to initiate synthesis of the nucleic acid molecule. For instance through random-primed reverse transcription. Also provided are modified random primers (such as amine-modified random primers) useful in these methods, labeling and hybridization kits comprising such primers, labeled nucleic acid molecules and mixtures of molecules, and methods for using them.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 7 OF 28 USPATFULL on STN
AN 2005:240538 USPATFULL
TI Methods for analysis of nucleic acid methylation status and methods for fragmentation, labeling and immobilization of nucleic acids
IN Kurn, Nurith, Palo Alto, CA, UNITED STATES
Dafforn, Geoffrey A., Los Altos, CA, UNITED STATES
PI US 2005208538 A1 20050922
AI US 2004-26280 A1 20041229 (11)
PRAI US 2003-533381P 20031229 (60)
DT Utility
FS APPLICATION
LREP MORRISON & FOERSTER LLP, 755 PAGE MILL RD, PALO ALTO, CA, 94304-1018, US
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 1 Drawing Page(s)
LN.CNT 3352
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to methods for analysis of nucleic acid methylation status, and fragmentation and/or labeling and/or immobilization of nucleic acids. More particularly, the invention relates to methods for fragmentation and/or labeling and/or immobilization of nucleic acids comprising labeling and/or cleavage and/or immobilization at abasic sites.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 8 OF 28 USPATFULL on STN
AN 2005:62950 USPATFULL
TI Compositions and methods for analysis of nucleic acids
IN Makarov, Vladimir L., Ann Arbor, MI, UNITED STATES

Langmore, John P., Ann Arbor, MI, UNITED STATES
PI US 2005053986 A1 20050310
AI US 2004-890483 A1 20040713 (10)
RLI Division of Ser. No. US 2001-801346, filed on 6 Mar 2001, GRANTED, Pat. No. US 6762022 Continuation of Ser. No. US 1998-151236, filed on 10 Sep 1998, GRANTED, Pat. No. US 6197557 Continuation-in-part of Ser. No. US 1998-35677, filed on 5 Mar 1998, ABANDONED
DT Utility
FS APPLICATION
LREP FULBRIGHT & JAWORSKI L.L.P., 600 CONGRESS AVE., SUITE 2400, AUSTIN, TX, 78701
CLMN Number of Claims: 21
ECL Exemplary Claim: CLM-1-104
DRWN 36 Drawing Page(s)
LN.CNT 5793
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed are a number of methods that can be used in a variety of embodiments, including, creation of a nucleic acid terminated at one or more selected bases, sequence analysis of nucleic acids, mapping of sequence motifs within a nucleic acid, positional mapping of nucleic acid clones, and analysis of telomeric regions. The methods utilize double-stranded templates, and in most aspects involve a strand replacement reaction initiated at one or more random or specific locations created in a nucleic acid molecule, and in certain aspects utilizing an oligonucleotide primer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 9 OF 28 USPATFULL on STN
AN 2005:62943 USPATFULL
TI Combinatorial nucleobase oligomers comprising universal base analogues and methods for making and using same
IN Livak, Kenneth J., San Jose, CA, UNITED STATES
Mullah, Khairuzzaman Bashar, Union City, CA, UNITED STATES
PI US 2005053979 A1 20050310
AI US 2004-866523 A1 20040610 (10)
PRAI US 2003-478678P 20030612 (60)
DT Utility
FS APPLICATION
LREP HELLER EHRMAN WHITE & MCAULIFFE LLP, 275 MIDDLEFIELD ROAD, MENLO PARK, CA, 94025-3506
CLMN Number of Claims: 76
ECL Exemplary Claim: 1
DRWN 11 Drawing Page(s)
LN.CNT 3701
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to insulating combinatorial nucleobase oligomers that comprise universal base analogs, where the oligomers are formed by the ligation of two or more oligomer "blocks" via a covalent linkage. Universal bases may serve to insulate specifically binding nucleobases from the effects of the covalent linker region joining two oligomer blocks together, so that the universal bases at least partially negate the T.sub.m penalty caused by the covalent linkage, effective to reduce the required minimal length of the oligomer blocks and the combinatorial oligomer. The resulting insulating nucleobase combinatorial oligomers find use in any hybridization-based application, including use as probes and primers. The combinatorial oligomers of the present invention provide advantages over existing combinatorial oligomer systems currently known in the art.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 10 OF 28 USPATFULL on STN
AN 2004:334806 USPATFULL

TI Binary encoded sequence tags
IN Kaufman, Joseph C., Hamden, CT, UNITED STATES
Roth, Matthew E., Branford, CT, UNITED STATES
Lizardi, Paul M., Wallingford, CT, UNITED STATES
Feng, Li, Hamden, CT, UNITED STATES
Latimer, Darin R., East Haven, CT, UNITED STATES
PA Horlick, Kenneth R. (U.S. corporation)
PI US 2004265888 A1 20041230
AI US 2004-872984 A1 20040621 (10)
RLI Continuation of Ser. No. US 2001-994311, filed on 26 Nov 2001, GRANTED, Pat. No. US 6773886 Continuation of Ser. No. US 2000-637751, filed on 11 Aug 2000, GRANTED, Pat. No. US 6383754 Continuation-in-part of Ser. No. US 2000-544713, filed on 6 Apr 2000, GRANTED, Pat. No. US 6261782
PRAI US 1999-148870P 19990813 (60)
DT Utility
FS APPLICATION
LREP NEEDLE & ROSENBERG, P.C., SUITE 1000, 999 PEACHTREE STREET, ATLANTA, GA, 30309-3915
CLMN Number of Claims: 126
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 3697
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Binary Encoded Sequence Tags (BEST), involves generation of a set of nucleic acid fragments; adding an adaptor to the ends containing recognition site for cleavage at a site offset from the recognition site; cleaving the fragment to generate fragments having a plurality sticky ends; indexing of the fragments into sets based on the sequence of sticky ends. The fragments are indexed by adding a offset adaptor to newly generated ends. A different adaptor will be coupled to each different sticky end. The resulting fragments--which will have defined ends, be of equal lengths (in preferred embodiment), and a central sequence derived from the source nucleic acid molecule--are binary sequence tags. The binary sequence tags can be used and further analyzed in numerous ways. For example, the binary sequence tags can be captured by hybridization and coupling, preferably by ligation, to a probe. The probe is preferably immobilized in an array or on sortable beads. One form of the BEST method, referred to as modification assisted analysis of binary sequence tags (MAABST), assesses modification of sequences in nucleic acid molecules by detecting differential cleavage based on the presence or absence of modification in the molecules.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 11 OF 28 USPATFULL on STN
AN 2003:244266 USPATFULL
TI Methods of manipulating nucleic acids
IN Xiang, Charlie, Germantown, MD, UNITED STATES
Brownstein, Michael J., Rockville, MD, UNITED STATES
PA The Gov't of the U.S of America as represented by the Secretary of the Dept. of Health & Human Serv. (U.S. corporation)
PI US 2003170675 A1 20030911
AI US 2002-269515 A1 20021011 (10)
RLI Continuation-in-part of Ser. No. WO 2002-US11656, filed on 11 Apr 2002, PENDING
PRAI US 2001-283423P 20010411 (60)
DT Utility
FS APPLICATION
LREP KLARQUIST SPARKMAN, LLP, One World Trade Center, Suite 1600, 121 S.W. Salmon Street, Portland, OR, 97204
CLMN Number of Claims: 57
ECL Exemplary Claim: 1

DRWN 7 Drawing Page(s)
LN.CNT 3279
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods are provided for labeling nucleic acid molecules for use in hybridization reactions, and kits employing these methods. The level of labeling is increased by including one or more reactive modifications, such as amine-modifications, into the primers used to initiate synthesis of the nucleic acid molecule, for instance through random-primed reverse transcription. Also provided are modified random primers (such as amine-modified random primers) useful in these methods, labeling and hybridization kits comprising such primers, labeled nucleic acid molecules and mixtures of molecules, and methods for using them. Methods are also provided for amplifying a nucleic acid template contained within extremely small samples, in some cases as little as one cell. In particular embodiments, a single random primer is used for all steps of the amplification method. The nucleic acid template can either be of cellular or viral origin.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 12 OF 28 USPATFULL on STN
AN 2003:120073 USPATFULL
TI Binary encoded sequence tags
IN Kaufman, Joseph C., Hamden, CT, UNITED STATES
Roth, Matthew E., Branford, CT, UNITED STATES
Lizardi, Paul M., Wallingford, CT, UNITED STATES
Feng, Li, Hamden, CT, UNITED STATES
Latimer, Darin R., East Haven, CT, UNITED STATES
PA Yale University (U.S. corporation)
PI US 2003082556 A1 20030501
US 6773886 B2 20040810
AI US 2001-994311 A1 20011126 (9)
RLI Continuation of Ser. No. US 2000-637751, filed on 11 Aug 2000, PENDING
Continuation-in-part of Ser. No. US 2000-544713, filed on 6 Apr 2000, PATENTED
PRAI US 1999-148870P 19990813 (60)
DT Utility
FS APPLICATION
LREP NEEDLE & ROSENBERG, P.C., Suite 1200, The Candler Building, 127 Peachtree Street, N.E., Atlanta, GA, 30303-1811
CLMN Number of Claims: 126
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 3686
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Binary Encoded Sequence Tags (BEST), involves generation of a set of nucleic acid fragments; adding an adaptor to the ends containing recognition site for cleavage at a site offset from the recognition site; cleaving the fragment to generate fragments having a plurality sticky ends; indexing of the fragments into sets based on the sequence of sticky ends. The fragments are indexed by adding a offset adaptor to newly generated ends. A different adaptor will be coupled to each different sticky end. The resulting fragments--which will have defined ends, be of equal lengths (in preferred embodiment), and a central sequence derived from the source nucleic acid molecule--are binary sequence tags. The binary sequence tags can be used and further analyzed in numerous ways. For example, the binary sequence tags can be captured by hybridization and coupling, preferably by ligation, to a probe. The probe is preferably immobilized in an array or on sortable beads. One form of the BEST method, referred to as modification assisted analysis of binary sequence tags (MAABST), assesses modification of sequences in nucleic acid molecules by detecting differential cleavage

based on the presence or absence of modification in the molecules.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 13 OF 28 USPATFULL on STN
AN 2003:78476 USPATFULL
TI Enzymatic light amplification
IN Weiner, Michael P., Guilford, CT, UNITED STATES
PI US 2003054396 A1 20030320
AI US 2002-236871 A1 20020906 (10)
PRAI US 2001-318218P 20010907 (60)
US 2001-335950P 20011030 (60)
DT Utility
FS APPLICATION
LREP MINTZ, LEVIN, COHN, FERRIS, GLOVSKY, AND POPEO, P.C., ONE FINANCIAL CENTER, BOSTON, MA, 02111
CLMN Number of Claims: 73
ECL Exemplary Claim: 1
DRWN 9 Drawing Page(s)
LN.CNT 3252
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Reversibly labeled nucleotides and methods involving the nucleotides are disclosed. The methods included methods of determining a sequence of a nucleic acid.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 14 OF 28 USPATFULL on STN
AN 2003:23647 USPATFULL
TI Method for detecting single nucleotide polymorphisms (SNP'S) and point mutations
IN Xue, Hong, New Territories, HONG KONG
Wong, Jeffrey Tze-Fei, Mid-Levels, HONG KONG
PA PharmacoGenetics, Ltd., Clear Water Bay, HONG KONG (non-U.S. corporation)
PI US 2003017487 A1 20030123
US 6972174 B2 20051206
AI US 2002-162530 A1 20020604 (10)
RLI Continuation-in-part of Ser. No. US 2001-876727, filed on 6 Jun 2001, PENDING
DT Utility
FS APPLICATION
LREP T. Ling Chwang, Suite 600, 2435 N. Central Expressway, Richardson, TX, 75080
CLMN Number of Claims: 83
ECL Exemplary Claim: 1
DRWN 12 Drawing Page(s)
LN.CNT 1562
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method of genotyping single nucleotide polymorphisms ("SNP") and point mutations in nucleic acid based on chain extension by polymerase. This invention is based on the fact that the nucleoside immediately 5' adjacent to any SNP/point mutation site is known, and the neighboring sequence immediately 3' adjacent to the site is also known. A primer complementary to the sequence directly adjacent to the SNP on the 3' side in a target polynucleotide is used for chain elongation. The polymerase reaction mixture contains one chain-terminating nucleotide having a base complementary to the nucleotide directly adjacent to the SNP on the 5' side in the target polynucleotide. An additional dNTP may be added to produce a primer with the maximum of a two-base extension. The resultant elongation/termination reaction products are analyzed for the length of chain extension of the primer, or for the amount of label incorporation from a labeled form of the terminator nucleotide.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 15 OF 28 USPATFULL on STN
AN 2003:17365 USPATFULL
TI Multiplexed differential displacement for nucleic acid determinations
IN Singh, Sharat, San Jose, CA, UNITED STATES
Inamdar, Anita, Sunnyvale, CA, UNITED STATES
Ullman, Edwin F., Atherton, CA, UNITED STATES
Cao, Liching, Vallejo, CA, UNITED STATES
Albagli, David, Millbrae, CA, UNITED STATES
PA ACLARA BioSciences, Inc. (U.S. corporation)
PI US 2003013117 A1 20030116
AI US 2002-245030 A1 20020916 (10)
RLI Continuation of Ser. No. US 2000-684590, filed on 5 Oct 2000, PENDING Continuation-in-part of Ser. No. US 2000-609279, filed on 30 Jun 2000, PENDING Continuation-in-part of Ser. No. US 1999-354629, filed on 16 Jul 1999, PENDING
DT Utility
FS APPLICATION
LREP PERKINS COIE LLP, P.O. BOX 2168, MENLO PARK, CA, 94026
CLMN Number of Claims: 48
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 1498
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Multiplexed determinations of large numbers of events are achieved in an accurate and simple manner by using a multitude of primer reagents in combination with different capture reagents that serve for sequestering all the reagents at a single site, followed by independent release of subsets of the primer reagents using differential release conditions. Also included as part of the primer reagents may be identifiers, which serve to identify a particular characteristic. The method is illustrated using primers with sequences for initiation of chain extension that are joined to or serve as a capture sequence, and where the extended primer has an identifier. After extending the primer, the extended primers are sequestered via the capture sequence onto a sequestering agent, sequentially released and the released extended primers analyzed to provide multiplexed determinations. The subject method finds application for nucleic acid sequencing, single nucleotide polymorphism determinations, identification of nucleic acid fragments, and the like.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 16 OF 28 USPATFULL on STN
AN 2002:235372 USPATFULL
TI Assay for genetic polymorphisms using scattered light detectable labels
IN Bee, Gary, Vista, CA, UNITED STATES
Kohne, David E., La Jolla, CA, UNITED STATES
Korb, Linda, San Diego, CA, UNITED STATES
Peterson, Todd, Coronado, CA, UNITED STATES
Yguerabide, Juan, La Jolla, CA, UNITED STATES
PI US 2002127561 A1 20020912
AI US 2001-880732 A1 20010612 (9)
PRAI US 2000-210988P 20000612 (60)
DT Utility
FS APPLICATION
LREP Wesley B. Ames, FOLEY & LARDNER, 23rd Floor, 402 West Broadway, San Diego, CA, 92101-3542
CLMN Number of Claims: 58
ECL Exemplary Claim: 1
DRWN 8 Drawing Page(s)
LN.CNT 2494
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Described are methods for determining the presence or absence of

particular polymorphisms in CYP2D6 and other genes using scattered light detectable particles as detectable labels, and compositions useful in such methods.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 17 OF 28 USPATFULL on STN
AN 2002:198549 USPATFULL
TI Fixed address analysis of sequence tags
IN Lizardi, Paul M., Wallingford, CT, UNITED STATES
Roth, Matthew E., Branford, CT, UNITED STATES
Feng, Li, Hamden, CT, UNITED STATES
Guerra, Cesar E., Guilford, CT, UNITED STATES
Weber, Shane C., Woodbridge, CT, UNITED STATES
Kaufman, Joseph C., Hamden, CT, UNITED STATES
Latimer, Darin R., East Haven, CT, UNITED STATES
PA Yale University (U.S. corporation)
PI US 2002106649 A1 20020808
US 6677121 B2 20040113
AI US 2001-855793 A1 20010515 (9)
RLI Continuation of Ser. No. US 2000-544713, filed on 6 Apr 2000, PATENTED
PRAI US 1999-127932P 19990406 (60)
DT Utility
FS APPLICATION
LREP Robert A. Hodges, NEEDLE & ROSENBERG, P.C., The Candler Building, Suite 1200, 127 Peachtree Street, N.E., Atlanta, GA, 30303-1811
CLMN Number of Claims: 154
ECL Exemplary Claim: 1
DRWN 5 Drawing Page(s)
LN.CNT 4340
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Fixed Address Analysis of Sequence Tags (FAAST), involves generation of a set of nucleic acid fragments having a variety of sticky end sequences; indexing of the fragments into sets based on the sequence of sticky ends; associating a detector sequence with the fragments; sequence-based capture of the indexed fragments on a detector array; and detection of the fragment labels. Generation of the multiple sticky end sequences is accomplished by incubating the nucleic acid sample with one or more nucleic acid cleaving reagents. The indexed fragments are captured by hybridization and coupling, preferably by ligation, to a probe. The method allows a complex sample of nucleic acid to be quickly and easily cataloged in a reproducible and sequence-specific manner. One form of the method allows determination of associations, in a nucleic acid molecule, of different combinations of known or potential sequences. Another form of the method assesses modification of sequences in nucleic acid molecules by basing cleavage of the molecules on the presence or absence of modification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 18 OF 28 USPATFULL on STN
AN 2002:102268 USPATFULL
TI Binary encoded sequence tags
IN Kaufman, Joseph C., Hamden, CT, United States
Roth, Matthew E., Branford, CT, United States
Lizardi, Paul M., Wallingford, CT, United States
Feng, Li, Hamden, CT, United States
Latimer, Darin R., East Haven, CT, United States
PA Yale University, United States (U.S. corporation)
Agilix Corporation, United States (U.S. corporation)
PI US 6383754 B1 20020507
AI US 2000-637751 20000811 (9)

RLI Continuation-in-part of Ser. No. US 2000-544713, filed on 6 Apr 2000, now patented, Pat. No. US 6261782
PRAI US 1999-148870P 19990813 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Needle & Rosenberg, P.C.
CLMN Number of Claims: 131
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 3871
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Binary Encoded Sequence Tags (BEST), involves generation of a set of nucleic acid fragments; adding an adaptor to the ends containing recognition site for cleavage at a site offset from the recognition site; cleaving the fragment to generate fragments having a plurality sticky ends; indexing of the fragments into sets based on the sequence of sticky ends. The fragments are indexed by adding a offset adaptor to newly generated ends. A different adaptor will be coupled to each different sticky end. The resulting fragments--which will have defined ends, be of equal lengths (in preferred embodiment), and a central sequence derived from the source nucleic acid molecule--are binary sequence tags. The binary sequence tags can be used and further analyzed in numerous ways. For example, the binary sequence tags can be captured by hybridization and coupling, preferably by ligation, to a probe. The probe is preferably immobilized in an array or on sortable beads. One form of the BEST method, referred to as modification assisted analysis of binary sequence tags (MAABST), assesses modification of sequences in nucleic acid molecules by detecting differential cleavage based on the presence or absence of modification in the molecules.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 19 OF 28 USPATFULL on STN
AN 2002:85142 USPATFULL
TI Multiplexed differential displacement for nucleic acid determinations
IN Singh, Sharat, San Jose, CA, UNITED STATES
Inamdar, Anita, Sunnyvale, CA, UNITED STATES
Ullman, Edwin F., Atherton, CA, UNITED STATES
Cao, Liching, Vallejo, CA, UNITED STATES
Albagli, David, Millbrae, CA, UNITED STATES
PA Lynx Therapeutics, Inc. (U.S. corporation)
PI US 2002045182 A1 20020418
AI US 2001-929333 A1 20010813 (9)
RLI Division of Ser. No. US 2000-684590, filed on 5 Oct 2000, PENDING Continuation-in-part of Ser. No. US 2000-609279, filed on 30 Jun 2000, PENDING Continuation-in-part of Ser. No. US 1999-354629, filed on 16 Jul 1999, PENDING
DT Utility
FS APPLICATION
LREP PERKINS COIE LLP, P.O. BOX 2168, MENLO PARK, CA, 94026
CLMN Number of Claims: 48
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 1497
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Multiplexed determinations of large numbers of events are achieved in an accurate and simple manner by using a multitude of primer reagents in combination with different capture reagents that serve for sequestering all the reagents at a single site, followed by independent release of subsets of the primer reagents using differential release conditions. Also included as part of the primer reagents may be identifiers, which

serve to identify a particular characteristic. The method is illustrated using primers with sequences for initiation of chain extension that are joined to or serve as a capture sequence, and where the extended primer has an identifier. After extending the primer, the extended primers are sequestered via the capture sequence onto a sequestering agent, sequentially released and the released extended primers analyzed to provide multiplexed determinations. The subject method finds application for nucleic acid sequencing, single nucleotide polymorphism determinations, identification of nucleic acid fragments, and the like.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 20 OF 28 USPATFULL on STN
AN 2002:78405 USPATFULL
TI Compositions and methods for analysis of nucleic acids
IN Makarov, Vladimir L., Ann Arbor, MI, UNITED STATES
Langmore, John P., Ann Arbor, MI, UNITED STATES
PA The Regents of the University of Michigan (U.S. corporation)
PI US 2002042059 A1 20020411
US 6762022 B2 20040713
AI US 2001-801346 A1 20010306 (9)
RLI Continuation of Ser. No. US 1998-151236, filed on 10 Sep 1998, GRANTED, Pat. No. US 6197557 Continuation-in-part of Ser. No. US 1998-35677, filed on 5 Mar 1998, ABANDONED Continuation-in-part of Ser. No. US 1997-811804, filed on 6 Mar 1997, GRANTED, Pat. No. US 6117634
DT Utility
FS APPLICATION
LREP David L. Parker, FULBRIGHT & JAWORSKI L.L.P., 600 Congress Avenue, Suite 2400, Austin, TX, 78701
CLMN Number of Claims: 104
ECL Exemplary Claim: 1
DRWN 38 Drawing Page(s)
LN.CNT 6552
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed are a number of methods that can be used in a variety of embodiments, including, creation of a nucleic acid terminated at one or more selected bases, sequence analysis of nucleic acids, mapping of sequence motifs within a nucleic acid, positional mapping of nucleic acid clones, and analysis of telomeric regions. The methods utilize double-stranded templates, and in most aspects involve a strand replacement reaction initiated at one or more random or specific locations created in a nucleic acid molecule, and in certain aspects utilizing an oligonucleotide primer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 21 OF 28 USPATFULL on STN
AN 2001:112050 USPATFULL
TI Fixed address analysis of sequence tags
IN Lizardi, Paul M., Wallingford, CT, United States
Roth, Matthew E., Branford, CT, United States
Feng, Li, Hamden, CT, United States
Guerra, Cesar E., Guilford, CT, United States
Weber, Shane C., Woodbridge, CT, United States
Kaufman, Joseph C., Hamden, CT, United States
Latimer, Darin R., East Haven, CT, United States
PA Yale University, New Haven, CT, United States (U.S. corporation)
PI US 6261782 B1 20010717
AI US 2000-544713 20000406 (9)
PRAI US 1999-127932P 19990406 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Needle & Rosenberg, P.C.

CLMN Number of Claims: 154
ECL Exemplary Claim: 1
DRWN 5 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 4505
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Fixed Address Analysis of Sequence Tags (FAAST), involves generation of a set of nucleic acid fragments having a variety of sticky end sequences; indexing of the fragments into sets based on the sequence of sticky ends; associating a detector sequence with the fragments; sequence-based capture of the indexed fragments on a detector array; and detection of the fragment labels. Generation of the multiple sticky end sequences is accomplished by incubating the nucleic acid sample with one or more nucleic acid cleaving reagents. The indexed fragments are captured by hybridization and coupling, preferably by ligation, to a probe. The method allows a complex sample of nucleic acid to be quickly and easily cataloged in a reproducible and sequence-specific manner. One form of the method allows determination of associations, in a nucleic acid molecule, of different combinations of known or potential sequences. Another form of the method assesses modification of sequences in nucleic acid molecules by basing cleavage of the molecules on the presence or absence of modification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 22 OF 28 USPATFULL on STN
AN 2001:33054 USPATFULL
TI Compositions and methods for analysis of nucleic acids
IN Makarov, Vladimir L., Ann Arbor, MI, United States
Langmore, John P., Ann Arbor, MI, United States
PA The Regents of the University of Michigan, Ann Arbor, MI, United States (U.S. corporation)
PI US 6197557 B1 20010306
AI US 1998-151236 19980910 (9)
RLI Continuation-in-part of Ser. No. US 1998-35677, filed on 5 Mar 1998, now abandoned Continuation-in-part of Ser. No. US 1997-811804, filed on 6 Mar 1997, now patented, Pat. No. US 6117634
DT Utility
FS Granted
EXNAM Primary Examiner: Brusca, John S.; Assistant Examiner: Kim, Young
LREP Fulbright & Jaworski, LLP
CLMN Number of Claims: 46
ECL Exemplary Claim: 1
DRWN 67 Drawing Figure(s); 38 Drawing Page(s)
LN.CNT 5768
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed are a number of methods that can be used in a variety of embodiments, including, creation of a nucleic acid terminated at one or more selected bases, sequence analysis of nucleic acids, mapping of sequence motifs within a nucleic acid, positional mapping of nucleic acid clones, and analysis of telomeric regions. The methods utilize double-stranded templates, and in most aspects involve a strand replacement reaction initiated at one or more random or specific locations created in a nucleic acid molecule, and in certain aspects utilizing an oligonucleotide primer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 23 OF 28 USPATFULL on STN
AN 2000:128125 USPATFULL
TI Nucleic acid amplification using single primer
IN Rose, Samuel, Mountain View, CA, United States
Goodman, Thomas C., Mountain View, CA, United States

Western, Linda M., Mountain View, CA, United States
Becker, Martin, Palo Alto, CA, United States
Ullman, Edwin F., Atherton, CA, United States
PA Behringwerke AG, Marburg, Germany, Federal Republic of (non-U.S. corporation)
PI US 6124090 20000926
AI US 1995-438149 19950509 (8)
RLI Division of Ser. No. US 1994-242931, filed on 16 May 1994 which is a continuation of Ser. No. US 1993-109852, filed on 20 Aug 1993, now abandoned which is a continuation of Ser. No. US 1991-734030, filed on 22 Jul 1991, now abandoned which is a continuation of Ser. No. US 1989-399795, filed on 29 Aug 1989, now abandoned which is a continuation-in-part of Ser. No. US 1989-299282, filed on 19 Jan 1989, now abandoned which is a division of Ser. No. US 1994-194140, filed on 9 Feb 1994, now patented, Pat. No. US 5508178 which is a continuation of Ser. No. US 1992-892412, filed on 1 Jun 1992, now abandoned which is a continuation of Ser. No. US 1989-299282, filed on 19 Jan 1989, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Zitomer, Stephanie W.; Assistant Examiner: Whisenant, Ethan
LREP Leitereg, Theodore J.
CLMN Number of Claims: 65
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 2173
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method is disclosed for determining the presence of a polynucleotide analyte in a sample suspected of containing the analyte. The method comprises (a) forming as a result of the presence of an analyte a single stranded polynucleotide comprising a target polynucleotide binding sequence flanked by first and second polynucleotide sequences that differ from the sequence of the analyte or a sequence complementary to the analyte sequence, (b) forming multiple copies of the single stranded polynucleotide, and (c) detecting the single stranded polynucleotide. Also disclosed is a method of producing at least one copy of a single stranded polynucleotide. The method comprises (a) forming in the presence of nucleoside triphosphates and template dependent polynucleotide polymerase an extension of a polynucleotide primer at least the 3'-end of which has at least a 10 base sequence hybridizable with a second sequence flanking the 3'-end of the single stranded polynucleotide, the second sequence being partially or fully complementary with at least a 10 base first sequence flanking the 5' end of the single stranded polynucleotide, (b) dissociating the extended polynucleotide primer and the single stranded polynucleotide, (c) repeating step a and (d) dissociating the extended polynucleotide primer and the copy of the single stranded polynucleotide.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 24 OF 28 USPATFULL on STN
AN 1998:131529 USPATFULL
TI Kits for nucleic acid amplification kit using single primer
IN Rose, Samuel, Mountain View, CA, United States
Goodman, Thomas C., Mountain View, CA, United States
Western, Linda M., Mountain View, CA, United States
Becker, Martin, Palo Alto, CA, United States
Ullman, Edwin F., Atherton, CA, United States
PA Behring Diagnostics GmbH, Deerfield, IL, United States (U.S. corporation)
PI US 5827649 19981027
AI US 1994-242931 19940516 (8)
RLI Continuation of Ser. No. US 1993-109852, filed on 20 Aug 1993, now

abandoned which is a continuation of Ser. No. US 1991-734030, filed on 22 Jul 1991, now abandoned which is a continuation of Ser. No. US 1989-399795, filed on 29 Aug 1989, now abandoned which is a continuation-in-part of Ser. No. US 1989-299282, filed on 19 Jan 1989, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Marschel, Ardin H.
LREP Leitereg, Theodore J.
CLMN Number of Claims: 5
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 1889
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method is disclosed for determining the presence of a polynucleotide analyte in a sample suspected of containing the analyte. The method comprises (a) forming as a result of the presence of an analyte a single stranded polynucleotide comprising a target polynucleotide binding sequence flanked by first and second polynucleotide sequences that differ from the sequence of the analyte or a sequence complementary to the analyte sequence, (b) forming multiple copies of the single stranded polynucleotide, and (c) detecting the single stranded polynucleotide. Also disclosed is a method of producing at least one copy of a single stranded polynucleotide. The method comprises (a) forming in the presence of nucleoside triphosphates and template dependent polynucleotide polymerase an extension of a polynucleotide primer at least the 3'-end of which has at least a 10 base sequence hybridizable with a second sequence flanking the 3'-end of the single stranded polynucleotide, the second sequence being partially or fully complementary with at least a 10 base first sequence flanking the 5' end of the single stranded polynucleotide, (b) dissociating the extended polynucleotide primer and the single stranded polynucleotide, (c) repeating step a and (d) dissociating the extended polynucleotide primer and the copy of the single stranded polynucleotide.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 25 OF 28 USPATFULL on STN
AN 97:22643 USPATFULL
TI Method for producing a polynucleotide for use in single primer amplification
IN Western, Linda M., San Mateo, CA, United States
Hahnenberger, Karen M., Cupertino, CA, United States
Rose, Samuel, Mountain View, CA, United States
Becker, Martin, Palo Alto, CA, United States
Ullman, Edwin F., Atherton, CA, United States
PA Behringwerke AG, Marburg, Germany, Federal Republic of (non-U.S. corporation)
PI US 5612199 19970318
AI US 1994-221662 19940401 (8)
RLI Continuation of Ser. No. US 1991-776538, filed on 11 Oct 1991, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Zitomer, Stephanie W.
LREP Leitereg, Theodore J.
CLMN Number of Claims: 46
ECL Exemplary Claim: 2
DRWN 8 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 1936
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method is disclosed for extending an extender probe to produce a single stranded polydeoxynucleotide that is free of unreacted extender probe and has two segments that are non-contiguous and complementary

with each other. The method comprises the steps of (1) providing in combination (a) a polynucleotide having two non-contiguous, non-complementary nucleotide sequences S1 and S2 wherein S2 is 5' of S1 and is at least ten deoxynucleotides long, (b) an extender probe comprised of two deoxynucleotide sequences, wherein the sequence at the 3'-end of the extender probe (EP1) is hybridizable with S1 and the other of the deoxynucleotide sequences (EP2) is substantially identical to S2 and (c) means for modifying the 3'-end of extender probe that does not hybridize with the polynucleotide and (2) extending the extender probe along the polynucleotide wherein extender probe not hybridized to the polynucleotide becomes modified at its 3'-end.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 26 OF 28 USPATFULL on STN
AN 97:5872 USPATFULL
TI Method for producing a polynucleotide for use in single primer amplification
IN Rose, Samuel, Mountain View, CA, United States
Western, Linda M., Mountain View, CA, United States
Becker, Martin, Palo Alto, CA, United States
Ullman, Edwin F., Atherton, CA, United States
PA Behringwerke AG, Marburg, Germany, Federal Republic of (non-U.S. corporation)
PI US 5595891 19970121
AI US 1990-555323 19900719 (7)
DT Utility
FS Granted
EXNAM Primary Examiner: Zitomer, Stephanie W.
LREP Leitereg, Theodore J.
CLMN Number of Claims: 49
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 2 Drawing Page(s)
LN.CNT 1793
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method is disclosed for producing a single stranded polydeoxynucleotide having two segments that are non-contiguous and complementary with each other. The method comprises the steps of providing in combination (1) a polynucleotide having two non-contiguous, non-complementary nucleotide sequences S1 and S2 wherein S2 is 5' of S1 and is at least ten deoxynucleotides long and (2) an extender probe comprised of two deoxynucleotide sequences, wherein the sequence at the 3'-end of the extender probe is hybridizable with S1 and the other of the deoxynucleotide sequences is homologous to S2 and (b) extending the extender probe along the polynucleotide. The method can also comprise providing in the combination a polydoxynucleotide primer capable of hybridizing at least at its 3'-end with a nucleotide sequence complementary to S2 under conditions where (1) the extended extender probe is rendered single stranded, (2) the polydeoxynucleotide primer hybridizes with and is extended along the extended extender probe to form a duplex comprising extended primer, (3) the extended primer is dissociated from the duplex, and (4) the primer hybridizes with and is extended along the extended primer to form a duplex comprising extended primer, and repeating steps (3) and (4). The method finds particular application in the detection of polynucleotide analytes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 27 OF 28 USPATFULL on STN
AN 96:31728 USPATFULL
TI Nucleic acid amplification using single primer
IN Rose, Samuel, 3401 Hillview Ave., P.O. Box 10850, Palo Alto, CA, United States 94303
Goodman, Thomas C., 3401 Hillview Ave., P.O. Box 10850, Palo Alto, CA,

United States 94303
Western, Linda M., 3401 Hillview Ave., P.O. Box 10850, Palo Alto, CA, United States 94303
Becker, Martin, 3401 Hillview Ave., P.O. Box 10850, Palo Alto, CA, United States 94303
Ullman, Edwin F., 3401 Hillview Ave., P.O. Box 10850, Palo Alto, CA, United States 94303
PI US 5508178 19960416
AI US 1994-194140 19940209 (8)
RLI Continuation of Ser. No. US 1992-892412, filed on 1 Jun 1992, now abandoned which is a continuation of Ser. No. US 1989-299282, filed on 19 Jan 1989, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Marschel, Ardin H.
LREP Leitereg, Theodore J.
CLMN Number of Claims: 25
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 4 Drawing Page(s)
LN.CNT 1860
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method is disclosed for determining the presence of a polynucleotide analyte in a sample suspected of containing the analyte. The method comprises (a) forming as a result of the presence of an analyte a single stranded polynucleotide comprising a target polynucleotide binding sequence flanked by first and second polynucleotide sequences that differ from the sequence of the analyte or a sequence complementary to the analyte sequence, (b) forming multiple copies of the single stranded polynucleotide, and (c) detecting the single stranded polynucleotide. Also disclosed is a method of producing at least one copy of a single stranded polynucleotide. The method comprises (a) forming in the presence of nucleoside triphosphates and template dependent polynucleotide polymerase an extension of a polynucleotide primer at least the 3'-end of which has at least a 10 base sequence hybridizable with a second sequence flanking the 3'-end of the single stranded polynucleotide, the second sequence being partially or fully complementary with at least a 10 base first sequence flanking the 5' end of the single stranded polynucleotide, (b) dissociating the extended polynucleotide primer and the single stranded polynucleotide, (c) repeating step a and (d) dissociating the extended polynucleotide primer and the copy of the single stranded polynucleotide.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 28 OF 28 USPATFULL on STN
AN 95:71247 USPATFULL
TI Method for producing a polynucleotide having an intramolecularly base-paired structure
IN Rose, Samuel, Mountain View, CA, United States
Western, Linda M., Mountain View, CA, United States
PA Syntex (U.S.A.) Inc., Palo Alto, CA, United States (U.S. corporation)
PI US 5439793 19950808
AI US 1990-555968 19900719 (7)
DT Utility
FS Granted
EXNAM Primary Examiner: Zitomer, Stephanie W.
LREP Leitereg, Theodore J.
CLMN Number of Claims: 49
ECL Exemplary Claim: 1
DRWN 4 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 2156
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method is disclosed for forming a single stranded polynucleotide having two segments that are non-contiguous and hybridizable with each

other. The method comprises the step of providing in combination (1) a first polynucleotide sequence having a hydroxyl at its 3'-end, (2) a second polynucleotide sequence having a hydroxyl or phosphate group at its 5'-end, and (3) a ligase, wherein at least ten consecutive bases of one of the sequences can hybridize to the other of the sequences to form a duplex. The duplex is comprised of a non-hybridized single stranded portion of one of the polynucleotide sequences containing one of the ends and at least five bases. The combination is provided under conditions for forming the duplex and ligating the ends within the duplex. The method finds particular application in the detection of polynucleotide analytes.